5620

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/520,901
Source:	PUTIO
Date Processed by STIC:	1/24/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

	SUGGESTED CORRECTION SERIAL NUMBER: 10/520, 90/
ERROR DETECTED	
ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
IWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
·2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid
-	AMC - Riotechnology Systems Branch - 09/09/2003



phose alig

1/24/05

PCT

RAW SEQUENCE LISTING DATE: 01/24/2005
PATENT APPLICATION: US/10/520,901 TIME: 10:01:10

Input Set : A:\PTO.YF.txt

```
Output Set: N:\CRF4\01242005\J520901.raw
      2 <110> APPLICANT: KANSAI TLO
      3 <120> TITLE OF INVENTION: Selective Replication of Tumor-specific Replication-
competent Adenovirus
W-->
              on Tumor Cells
      5 <130> FILE REFERENCE: 42002JP
W-->
      6 <140> CURRENT APPLICATION NUMBER: 10/520,901
                                                                  Does Not Comply
Carrected Diskette Needer
      7 <141> CURRENT FILING DATE: 2005-01-07
      8 <160> NUMBER OF SEQ ID: 8
      9 <170> SOFTWARE: PatentIn Ver. 2.1
                                   invalid response- see ten 10 on Evor Su
     11 <210> SEQ ID NO: 1
     12 <211> LENGTH: 899
     13 <212> TYPE: DNA
     14 <213 > ORGANISM: (293 cell
W--> 15 <400> SEQUENCE: I
     16 acaccgggac tgaaaatgag acatattatc tgccacggag gtgttattac cgaagaaatg
                                                                             60
     17 gccgccagtc ttttggacca gctgatcgaa gaggtactgg ctgataatct tccacctcct
                                                                             120
                                                                              180
     18 agccattttg aaccacctac cettcacgaa etgtatgatt tagacgtgac ggcccccqaa
     19 gatcccaacg aggaggcggt ttcgcagatt tttcccgact ctgtaatgtt ggcggtgcag
                                                                               240
     20 gaagggattg acttactcac ttttccgccg gcgcccggtt ctccggagcc gcctcacctt
                                                                               300
     21 teceggeage eegageagee ggageagaga geettgggte eggtttetat geeaaacett
                                                                             360
     22 gtaccggagg tgatcgatct tacctgccac gaggctggct ttccacccag tgacgacgag
                                                                              420
     23 gatgaagagg gtgaggagtt tgtgttagat tatgtggagc accccgggca cggttgcagg
                                                                              480
     24 tettgteatt ateaceggag gaataegggg gaeceagata ttatgtgtte getttgetat
                                                                                540
     25 atgaggacct gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
                                                                               600
     26 ccagaacegg agcetgcaag acetaceege egtectaaaa tggegeetge tateetgaga
                                                                             660
     27 cgcccgacat cacctgtgtc tagagaatgc aatagtagta cggatagctg tgactccggt
                                                                              720
     28 cettetaaca caceteetga gatacaceeg gtggteeege tgtgeeecat taaaceagtt
                                                                               780
     29 gccgtgagag ttggtgggcg tcgccaggct gtggaatgta tcgaggactt gcttaacgag
                                                                             840
     30 cctgggcaac ctttggactt gagctgtaaa cgccccaggc cataaggtgt aaacctgtg
     32 <210> SEQ ID NO: 2
     33 <211> LENGTH: 1823
     34 <212> TYPE: DNA
     35 <213 > ORGANISM: (293 cell) Some env
W--> 36 <400> SEQUENCE: 2
     37 ctgacctcat ggaggcttgg gagtgtttgg aagatttttc tgctgtgcgt aacttgctgg
     38 aacagagete taacagtace tettggtttt ggaggtttet gtggggetea teceaggeaa
                                                                                    120
     39 agttagtetg cagaattaag gaggattaca agtgggaatt tgaagagett ttgaaateet
                                                                                    180
     40 gtggtgagct gtttgattct ttgaatctgg gtcaccaggc gcttttccaa gagaaggtca
                                                                                    240
     41 tcaagacttt ggatttttcc acaccggggc gcgctgcggc tgctgttgct tttttgagtt
                                                                                       300
     42 ttataaagga taaatggagc gaagaaaccc atctgagcgg ggggtacctg ctggattttc
                                                                                   360
     43 tggccatgca tctgtggaga gcggttgtga gacacaagaa tcgcctgcta ctgttgtctt
                                                                                    420
     44 cegteegeee ggegataata eegaeggagg ageageagea geageaggag gaageeagge
                                                                               480
     45 ggcggcggca ggagcagagc ccatggaacc cgagagccgg cctggaccct cgggaatgaa
                                                                               540
     46 tgttgtacag gtggctgaac tgtatccaga actgagacgc attttgacaa ttacagagga
                                                                                   600
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/520,901

DATE: 01/24/2005 TIME: 10:01:10

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01242005\J520901.raw

			ctaaaggggg					660	
	48	taggaatcta	gcttttagct	taatgaccag	acaccgtcct	gagtgtatta	cttttcaaca	720	\
	49	gatcaaggat	aattgcgcta	atgagcttga	tctgctggcg	cagaagtatt	ccatagagca	/780	\
	50	gctgaccact	tactggctgc	agccagggga	tgattttgag	gaggctatta	gggtatatgc	/ 840	,
	51	aaaggtggca	cttaggccag	attgcaagta	caagatcagc	aaacttgtaa	atatcaggaa	/ 900	
	52	ttgttgctac	atttctggga	acggggccga	ggtggagata	gatacggagg	atagggtggc	960	
	53	ctttagatgt	agcatgataa	atatgtggcc	gggggtgctt	ggcatggacg	gggtggttat	1020	
			aggtttactg					1080	
			cacggtgtaa					1140	
			gttcggggct					1200	
			gcttcaatta					1260	
			tccagggtgc					1320	
			gctgtgatta					1380	
			acctgctcgg					1440	
			aaggcctggc					1500	
			aggaggggg					. 1560	
			cccgagagca					1620	
			aaggtgctga					1680	
			catattagga					1740	/
			gtgctggcct					1800	
			gaaatgtgtg		3 3 33		5 5	1823	
		<210> SEQ :						<u> </u>	
	70	<211> LENG	TH: 605						
	71	<212> TYPE	: DNA						
	72	<213> ORGA	NISM: 293 C	ell)					
W>		<400> SEQUI							
	74	tgcatctagg	gcggccaatt	ccgcccctct	céctcccccc	cccctaacqt	tactggccga	60 🗻	
			aataaggccg					120	
			atgtgagggc					180	
			ctctcgccaa					240	\
			cttcttgaag					300	1
			gcgacaggtg					360	1
			aaccccagtg					\ 420	
			gcgtattcaa					480	/
	82	ggatctgatc	tggggcctcg	gtgcacatgc	tttacatgtg	tttagtcgag	gttaaaaaaa	540	
	83	cgtctaggcc	ccccgaacca	cggggacgtg	gttttccttt	gaaaaacacg	atgataagge	600	
	84	tgcca					605	? \	
	86	<210> SEQ 1	ID NO: 4						
•	87	<211> LENGT	ΓH: 455						
	88	<212> TYPE:	: DNA						
	89	<213> ORGAN	NISM: (293 ce	ell <i>)</i>					
W>		<400> SEQUE							
	91	tggcccctcc	ctcgggttac	cccacagcct	aggccgattc	gacctctctc	cactagaacc	60	
	92	ctcgctggcg	tccctgcacc	ctgggagcgc	qaqcqqcqcq	cgggcgggga	agcgcggccc	120	
			gtccgcccgg					180	
			cagacgccca					240	
			tgccccttca					300	
			ccgggtcccc					360	
	97	tttccgcggc	cccgccctct	cctcqcqqca	cgagtttcag	gcagcgctgc	gtcctactac	420	
•		5 55	_	- 3-33-3	JJ	J J - J - J -	5		



PATENT APPLICATION: US/10/520,901

DATE: 01/24/2005 TIME: 10:01:10

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01242005\J520901.raw

	98 gcacgtggga agccctggcc ccggccaccc ccgcg		455
	100 <210> SEQ ID NO: 5		
	101 <211> LENGTH: 20		
	102 <212> TYPE: DNA		
	103 <213> ORGANISM 293 cell		
W>	104 <400> SEQUENCE: 5		
	105 acaccgggac tgaaaatgag	20	
	107 <210> SEQ ID NO: 6		
	108 <211> LENGTH: 21		
	109 <212> TYPE: DNA		
	110 <213> ORGANISM: (293 cell)		
W>	111 <400> SEQUENCE: 6		
	112 cacaggttta caccttatgg c	21	
	114 <210> SEQ ID NO: 7		
	115 <211> LENGTH: 20		
	116 <212> TYPE: DNA		
	117 <213> ORGANISM: 293 cell		
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	119 ctgacctcat ggaggcttgg	20	
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	123 <212> TYPE: DNA		
	124 <213> ORGANISM: 293 cell)		
W>	125 <400> SEQUENCE: 8		
	126 gcccacacat ttcagtacct c	21	
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/520,901

DATE: 01/24/2005 TIME: 10:01:11

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01242005\J520901.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

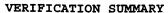
Seq#:1; Line(s) 3

Seq#:2; Line(s) 37,38,39,40,41,42,43,46,48,49,50,53,54,55,56,57,58,61,62,63

Seq#:2; Line(s) 66

Seq#:3; Line(s) 74,75,76,77,81,82,83

Seq#:4; Line(s) 91,95,97



PATENT APPLICATION: US/10/520,901

DATE: 01/24/2005 TIME: 10:01:11

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01242005\J520901.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:283 W: Missing Blank Line separator, <140> field identifier
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <400> field identifier
L:73 M:283 W: Missing Blank Line separator, <400> field identifier
L:90 M:283 W: Missing Blank Line separator, <400> field identifier
L:104 M:283 W: Missing Blank Line separator, <400> field identifier
L:111 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:283 W: Missing Blank Line separator, <400> field identifier
L:125 M:283 W: Missing Blank Line separator, <400> field identifier